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/translation="MASSGWTRRDPLAWKVALVTASTDGIGFAIARRLAQDGAHVVVS
SRKQQNVDQAVALQGEGLSYTGTVCHVGRAEDRERLVAMAVKLHGGIDILVSNAAVN
PFFGSLMDVTEEVWDKTLDINVKAFALMTKAVVPEMEKRGGGSVVIVSSIAAFSPSPG
FSPYNVSKTALLGLTKTLAIELAPRNIRVNCLAPGLIKTSFSRMLWMDKEKEESMKET
1235. 1240
                                                                                                                                                                                                                              PRI 27-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identification of peroxisomal proteins by using M13 phage protein VI phage display: molecular evidence that mammallan peroxisomes contain a 2.4-dienoyl-CoA reductase Biochem. J. 340 (Pt 2), 561-568 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1281)
Fransen,M., Van Veldhoven,P.P. and Subramani,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product-"peroxisomal short-chain alcohol dehydrogenase"
/protein_id-"AAD02292.1"
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2 (bases 1 to 1281)
Fransen,M. and Surbramani,S.
Direct Submission Nathernanission Submitred (22-74N-1998) Biology, University of California, San
Submitted (22-74N-1998) Biology, University of California, San
Diego, Gilman Drive, La Jolla, CA 92093-0322, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"SCAD-SRLp; contains a C-terminal peroxisomal targeting signal (PTS1)"
                                                                                                                                                                                                  1281 bp mRNA linear PRI 27. RPMS Sablens peroxisomal short-chain alcohol dehydrogenase (SCAD-SRL) mRNA, complete cds.
Percent Identity: 99.281
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                                                                                  267 rvalvalvalGlyGlyGlyThrProSerArgLeu 278
                                                                                                                            821 AGTGGTGGTGGTGGAGGAACCCCGTCCCGCCTC 854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'organism="Homo sapiens"
'db_xref="taxon:9606"
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323 c 395 g
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Percent Similarity: 99.640
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US-09-866-034-2 x AF044127
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                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                      seq_name: gb_pr:AF044127
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VERSION
KEYWORDS
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TITLE
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1 MetHisLysAlaGlyLeuLeuGlyLeuCysAlaArgAlaTrpAsnSerVa 17

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AB062757 880 bp mRNA linear MAM 04-DEC-2001
Sus scrofa mRNA for carbonyl reductase/NADP-retinol dehydrogenase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         250
                                                                                                                                                                                               175
                                                                                                                                                                                                                                                                                            117 aAlaValAsnProPhePheGlySerIleMetAspValThrGluGluValT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         376 TGCTGTCAACCCTTTCTTTGGAAGCCTAATGGATGTCACTGAGGAGGTGT 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 AlaValValProGluMetGluLysArgGlyGlyGlySerValValIleVa 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167 ISerSerIleAlaAlaPheSerProSerProGlyPheSerProTyrAsnV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201 AlaProArgAsnIleArgValAsnCysLeuAlaProGlyLeuIleLysTh 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              626 GCCCCAAGGAACATTAGGGTGAACTGCCTAGCACCTGGACTATCAAGAC 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  217 rSerPheSerArgMetLeuTrpMétAspLysGluLysGluGluSerMetL 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       676 TAGCTTCAGCAGGATGCTCTGGATGGACAAGGAAAAAGAGGAAAGCATGA 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               251 IleValSerPheLeuCysSerGluAspAlaSerTyrIleThrGlyGluTh 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            776 ATCGTGTCTTTCCTGTGCTCTGAAGATGCCAGCTACATCACTGGGGAAAC 825
                                                                                                                                                                                                                                                                          67 nAsnvalAspGlnAlavalAlaThrLeuGlnGlyGluGlyLeuServalT 84
                    26 ATGCACAGAGGCGGGGCTGCTAGGCCTTGTGTGCCCGGGCTTGGAATTCGGT 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234 ysGluThrLeuArgIleArgArgLeuGlyGluProGluAspCysAlaGly
                                                                                                                           34 alAlaLeuValThrAlaSerThrAspGlyIleGlyPheAlaIleAlaArg
                                                                                                                                                                 126 TGGCCCTGGTAACGGCCTCCACCGACGGGATCGGCTTCGCCATCGCCCGG
267 rvalyalvalGlyGlyGlyThrProSerArgLeu 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seg_documentation_block:
LOCUS AB062757
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